

SID 59

RESULT 10
E34283
LOCUS E34283 941 bp DNA linear PAT 31-JAN-2002
DEFINITION Environmental stress-tolerant plant.
ACCESSION E34283
VERSION E34283.1 GI:18624288
KEYWORDS JP 2000116259-A/12.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 941)
AUTHORS Shinozaki, K. and Kasuga, M.
TITLE Environmental stress-tolerant plant
JOURNAL Patent: JP 2000116259-A 12 25-APR-2000;
JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES,
BIO-ORIENTED TECHNOL RES ADVANCEMENT INST
COMMENT OS Arabidopsis thaliana
PN JP 2000116259-A/12
PD 25-APR-2000
PF 09-OCT-1998 JP 1998287999
PR
PI KAZUKO SHINOZAKI, MIE KASUGA
PC A01H5/00, C07K14/415, C12N5/10, C12N15/09, C12P21/02// (C12N15/09,
PC C12R1:91),
PC (C12P21/02, C12R1:19), C12N5/00, C12N15/00, (C12N15/00, C12R1:91)
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FH Key Location/Qualifiers
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FT /organism='Arabidopsis thaliana'.
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source 1. .941
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BASE COUNT 372 a 144 c 140 g 285 t
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Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20
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Db 632 ATATCATACCGACATCAGTT 651

RESULT 11
E34339
LOCUS E34339 941 bp DNA linear PAT 31-JAN-2002
DEFINITION Environmental stress-tolerant plant.
ACCESSION E34339
VERSION E34339.1 GI:18624324
KEYWORDS JP 2000116260-A/12.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 941)
AUTHORS Shinozaki,K. and Kasuga,M.
TITLE Environmental stress-tolerant plant
JOURNAL Patent: JP 2000116260-A 12 25-APR-2000;
JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES,
BIO-ORIENTED TECHNOL RES ADVANCEMENT INST

COMMENT OS Arabidopsis thaliana
PN JP 2000116260-A/12
PD 25-APR-2000
PF 14-OCT-1998 JP 1998292348
PR
PI KAZUKO SHINOZAKI,MIE KASUGA
PC A01H5/00,C07K14/415,C12N15/09,C12N15/00
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BASE COUNT 372 a 144 c 140 g 285 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20
|||||||
Db 632 ATATCATACCGACATCAGTT 651

RESULT 12
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LOCUS ATLTI78 3420 bp DNA linear PLN 16-MAR-1993
DEFINITION A.thaliana lti78 gene.
ACCESSION X67671
VERSION X67671.1 GI:16389
KEYWORDS lti78 gene.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 3420)
AUTHORS Vahala,T.K.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1992) T.K. Vahala, Swedish Univ. of Agricultural
Sciences, Dept. of Molecular Genetics, Box 7003, 75007 Uppsala,
SWEDEN

REFERENCE 2 (bases 1 to 3420)
AUTHORS Nordin,K., Vahala,T. and Palva,E.T.

TITLE Differential expression of two related, low-temperature-induced
 genes in *Arabidopsis thaliana* (L.) Heynh
 JOURNAL Plant Mol. Biol. 21 (4), 641-653 (1993)
 MEDLINE 93192524
 FEATURES

	Location/Qualifiers
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TATA_signal	770. .775 /note="putative"
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mRNA	join(803. .932,1018. .1200,1297. .1770,1855. .>3281) /gene="lti78"
gene	803. .3281 /gene="lti78"
CDS	join(884. .932,1018. .1200,1297. .1770,1855. .3281) /gene="lti78" /codon_start=1 /protein_id="CAA47903.1" /db_xref="GI:16390" /db_xref="SWISS-PROT:Q06738" /translation="MDQTEEPPLNTHQQHPVEVEHHENGATKMFRKVKARAKKFKNSL TKHGQSNEHEQDHDLVEEDDDDDDELEPEVIDAPGVTGKPRETNVPASEEIIIPPGTKVF PVSDDYTKPTESVPVQGEASYGHDAPAHSVRTTFTSDKEEKRDVPIHHPLSELSDREE SRETHHESLNTFPVSLLSGTEDVTSTFAPSGDDEYLDGQRKVNVPITILEEESAVSDY LSGVSNYQSKVTDPTKEETGGVPEIAESFGNMEVTDESPDQKPGQFERDLSTRSKEFK EFDQDFDSVLGKDSPA KFPGESGVVFPVGFGEDESGAELEKDFPTRSHDFDMKTETGMD TNSPSRSHEFDLKTESGNDKNSPMGFGSESGAELEKEFDQKNDSGRNEYSPESDGGLG APLGGNFPVRSHELDLKNESDIDKDVPTGFDGEPDFLAKGRPGYGEASEEDKFPARSD DVEVETELGRDPKTETLDQFSPELSHPKERDEFKESRDDFEETRDEKTEEPKQSTYTE KFASMLGYSGEIPVGDQTVAGTVDEKLTPVNEKDQETESAVTTKLPISGGGSGVEEQ RGEDKSVSGRDYVAEKLTTTEEDKAFSDMVAEKLQIGGEEKKETTTKEVEKISTEKA ASEEGEAVEEEVKGGGGMVGRIKGWFGGGATDEVKPESPHSVVEEAPKSSGWFGGGATE EVKPKSPHSVEESPQSLGSTVVPVQKEL"
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20
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 Db 574 ATATCATACCGACATCAGTT 593

RESULT 13
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LOCUS ATHCOR78B 3533 bp DNA linear PLN 30-SEP-1993
 DEFINITION Arabidopsis thaliana cor78 protein gene, complete cds.
 ACCESSION L22568
 VERSION L22568.1 GI:404667
 KEYWORDS cor78 gene.
 SOURCE Arabidopsis thaliana DNA.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 3533)
 AUTHORS Horvath,D.P., McLarney,B.K. and Thomashow,M.F.
 TITLE Cor78 genomic sequence
 JOURNAL Unpublished (1993)

FEATURES Location/Qualifiers
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 exon 809. .936
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 CDS join(888. .936,1022. .1204,1300. .1772,1857. .3284)
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 exon 1022. .1204
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 intron 1205. .1299
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 exon 1300. .1772
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 intron 1773. .1856
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 exon 1857. .3533
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BASE COUNT 1168 a 564 c 848 g 953 t
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Query Match 100.0%; Score 20; DB 8; Length 3533;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20
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 Db 577 ATATCATACCGACATCAGTT 596

RESULT 14

D13044

LOCUS D13044 8048 bp DNA linear PLN 14-APR-2000

DEFINITION Arabidopsis thaliana DNA for RD29B, RD29A, complete cds.

ACCESSION D13044

VERSION D13044.1 GI:285614

KEYWORDS RD29A; RD29B.

SOURCE Arabidopsis thaliana (strain:Columbia) DNA.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (sites)

AUTHORS Yamaguchi-Shinozaki,K. and Shinozaki,K.

TITLE Arabidopsis DNA encoding two desiccation-responsive rd29 genes

JOURNAL Plant Physiol. 101 (3), 1119-1120 (1993)

MEDLINE 94143472

REFERENCE 2 (bases 1 to 8048)

AUTHORS Shinozaki, K.

TITLE Direct Submission

JOURNAL Submitted (25-AUG-1992) Kazuo Shinozaki, Tsukuba Life Science Center, The Institute of Physical and Chemical Research; 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
(E-mail:sinozaki@rtc.riken.go.jp, Tel:0298-36-4359, Fax:0298-36-9060)

FEATURES

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exon	1997. .2108 /gene="rd29B" /number=2
exon	2222. .2736 /gene="rd29B" /number=3
exon	2813. .3927 /gene="rd29B" /number=4
TATA_signal	5398. .5403
gene	5512. .7909 /gene="rd29A"
CDS	join(5512. .5560, 5646. .5828, 5925. .6398, 6483. .7909) /gene="rd29A" /codon_start=1 /product="RD29A" /protein_id="BAA02376.1" /db_xref="GI:303504" /translation="MDQTEEPPLNTHQQHPVEVEHHENGATKMFRKVKARAKKFKNSL TKHGQSNEHEQDHDLDVEEDDDDDLEPEVIDAPGVTGKPRETNVPASEEIIPPGTVF PVVSSDYTKPTESVPVQEASYGHDAPAHSVRTTFTSDKEEKRDVPIHHPLSELSDREE"

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exon      5925. .6398
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ORIGIN

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Query Match      100.0%; Score 20; DB 8; Length 8048;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 atatcataccgacatcagtt 20
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Db      5201 ATATCATACCGACATCAGTT 5220

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RESULT 15
AB019226
LOCUS      AB019226      73999 bp      DNA      linear      PLN 27-DEC-2000
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24M7.
ACCESSION  AB019226 BA000015
VERSION    AB019226.1 GI:3869065
KEYWORDS   .
SOURCE     Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC
           clone:K24M7.
ORGANISM   Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (sites)
AUTHORS    Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E., Kotani,H.
           and Tabata,S.
TITLE      Structural analysis of Arabidopsis thaliana chromosome 5. X.
           Sequence features of the regions of 3,076,755 bp covered by sixty
           P1 and TAC clones
JOURNAL    DNA Res. 7 (1), 31-63 (2000)
MEDLINE    20181125
REFERENCE  2 (bases 1 to 73999)

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AUTHORS Nakamura, Y.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel: 81-438-52-3935, Fax: 81-438-52-3934)

COMMENT Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K24M7
 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi>).
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
 The 5' clone is F17P19 and the 3' clone is T4M5.

FEATURES

source Location/Qualifiers
 1. .73999
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 /strain="Columbia"
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 /clone="K24M7"
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CDS
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KLPHKSKVERTQKYHVPEESVDLFSSVCRYGAREDSRSVMTDSSSSSVSSGPDSDTHHV
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CDS
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APLGGNFPVRSHDLK NESDIDKDVPTGFDGEPDFLAKGRPGYGEASEEDKFPARSD
DVEVETELGRDPKTETLDQFSPELSHPKERDEFKESRDDFEETRDEKTEEPKQSTYTE
KFASMLGYSGEIPVGDQTVAGTVDEKLTPVNEKDQETESAVTTKLPI SGGGSGVEEQ
RGEDKSVSGRDYVAEKL TTEEDKAFSDMVAEKLQIGEEEEKETT TKEVEKISTEKA
ASEEGEAVEEEVKGGGMVGRIKGWFGGGGATDEVKPESPHSVVEEAPKSSGWFGGGGATE
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CDS
complement(16832. .18340)

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complement(join(19317. .19446,19535. .19638,19746. .20115,
20268. .20423,20568. .20700,20771. .20839,20931. .21019,
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DVILKGFVKHFFMENVTSPIAMDCLYNGLKDLEVTQKNKKASPKLLDDKELPAPFVK
VDRDMFVLVDDDDVLLLLLERAALLERAPEPLPPKDDKALQNRKEDKDEEDINKEAYE
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join(22523. .22681,22730. .22795,22845. .22940,23321.
.23526,
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strong similarity to unknown protein"
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LSKLEDEFQRQILQYNSKPMEPDRLFECPLPSNLRPSSEGE GGGGKTHDPHKSLENAIF
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VQRMQWEVLEAKIGNWIHYMRISVKLLFAAEKKICDQILDGVESLRDQCFGEVTVNSV
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FDSKDPDSELGAVTTRIMHALQNNLDEPEKPKHNPELELHFSQILQCLTVQSSGSGPI
ENSNISRASVKDRFKTFNSQFEELHQRCQWTVPDSELRESRLAVA EVLLPAFRSFL
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join(26632. .26954,27047. .27277,27393. .27531,27629.
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LPVLHDLAQQMVKAGHQQELFKTYRDIRRAVLAQSLEKLGVERHSKYDVERMNQDVFE
AKIMNWIHYIRISVKLLFAAEKEICHQILDGVEPFRDQSFAEITTISFGMLLSFGYAI

Query Match 100.0%; Score 20; DB 8; Length 73999;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20
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Db 12340 ATATCATACCGACATCAGTT 12359

RESULT 10

AAA53425

ID AAA53425 standard; DNA; 941 BP.

XX

AC AAA53425;

XX

DT 04-OCT-2000 (first entry)

XX

DE Rd29A gene fragment nucleotide sequence.

XX

KW Dehydration responsive element; DRE; transgenic plant; stress; salinity;

KW environmental stress; temperature; stress resistant plant; PCR primer;

KW rd29A; ds.

XX

OS Arabidopsis thaliana.

XX

PN JP2000116260-A.

XX

PD 25-APR-2000.

XX

PF 14-OCT-1998; 98JP-0292348.

XX

PR 14-OCT-1998; 98JP-0292348.

XX

PA (NORQ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.

PA (SEIB-) SEIBUTSUKAI TOKUTEI SANGYO GIJUTSU.

XX

DR WPI; 2000-389819/34.

XX

PT New transgenic plants resistant to environmental stresses, comprise a

PT DNA bound with a gene encoding for a transcription factor in a stress

PT responsive promoter -

XX

PS Example 5; Page 26; 36pp; Japanese.

XX

CC This invention relates to transgenic plants that are resistant to
CC environmental stresses. This sequence represents a fragment of an rd29A
CC gene used in the production of the transgenic plants of the invention.

CC The transgenic plants comprise a vector containing a gene encoding a
CC transcription factor and a stress responsive element (e.g. DRE

CC dehydration responsive element or rd29A promoter sequence). The

CC transcription factor gene is linked to the stress responsive element.

CC Also included in the invention is a method for the preparation of the

CC transgenic plants. This method can be used to prepare stress resistant

CC agricultural plants, which are resistant to dehydration, low temperature

CC and salinity.

XX

SQ Sequence 941 BP; 372 A; 144 C; 140 G; 285 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 941;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20

|||||

Db 632 atatcataccgacatcagtt 651

RESULT 11

AAA53474

ID AAA53474 standard; DNA; 941 BP.

XX

AC AAA53474;

XX

DT 04-OCT-2000 (first entry)

XX

DE Rd29A promoter nucleotide sequence.

XX

KW Dehydration responsive element; DRE; transgenic plant; stress; salinity;

KW environmental stress; temperature; stress resistant plant; rd29A;

KW promoter; ss.

XX

OS Arabidopsis thaliana.

XX

PN JP2000116259-A.

XX

PD 25-APR-2000.

XX

PF 09-OCT-1998; 98JP-0287999.

XX

PR 09-OCT-1998; 98JP-0287999.

XX

PA (NORQ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.

PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.

XX

DR WPI; 2000-379177/33.

XX

PT Plants resistant to environmental stresses. -

XX

PS Example 5; Page 26; 36pp; Japanese.

XX

CC The invention relates to transgenic plants resistant to environmental
CC stress. The plants comprise a vector containing a gene downstream of a
CC stress responsive element e.g. the stress responsive promoter of rd29A or
CC a dehydration responsive element (DRE). Also included in the invention is
CC a method for the production of the transgenic plants. This method can be
CC used to prepare stress resistant agricultural plants, which are resistant
CC to dehydration, can withstand low temperatures and environments of high
CC salinity.

CC The present sequence represents the promoter of the rd29A gene. The PCR
CC product is used in the production of the plants of the invention.

XX

SQ Sequence 941 BP; 372 A; 144 C; 140 G; 285 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 941;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20

|||||

Db 632 atatcataccgacatcagtt 651